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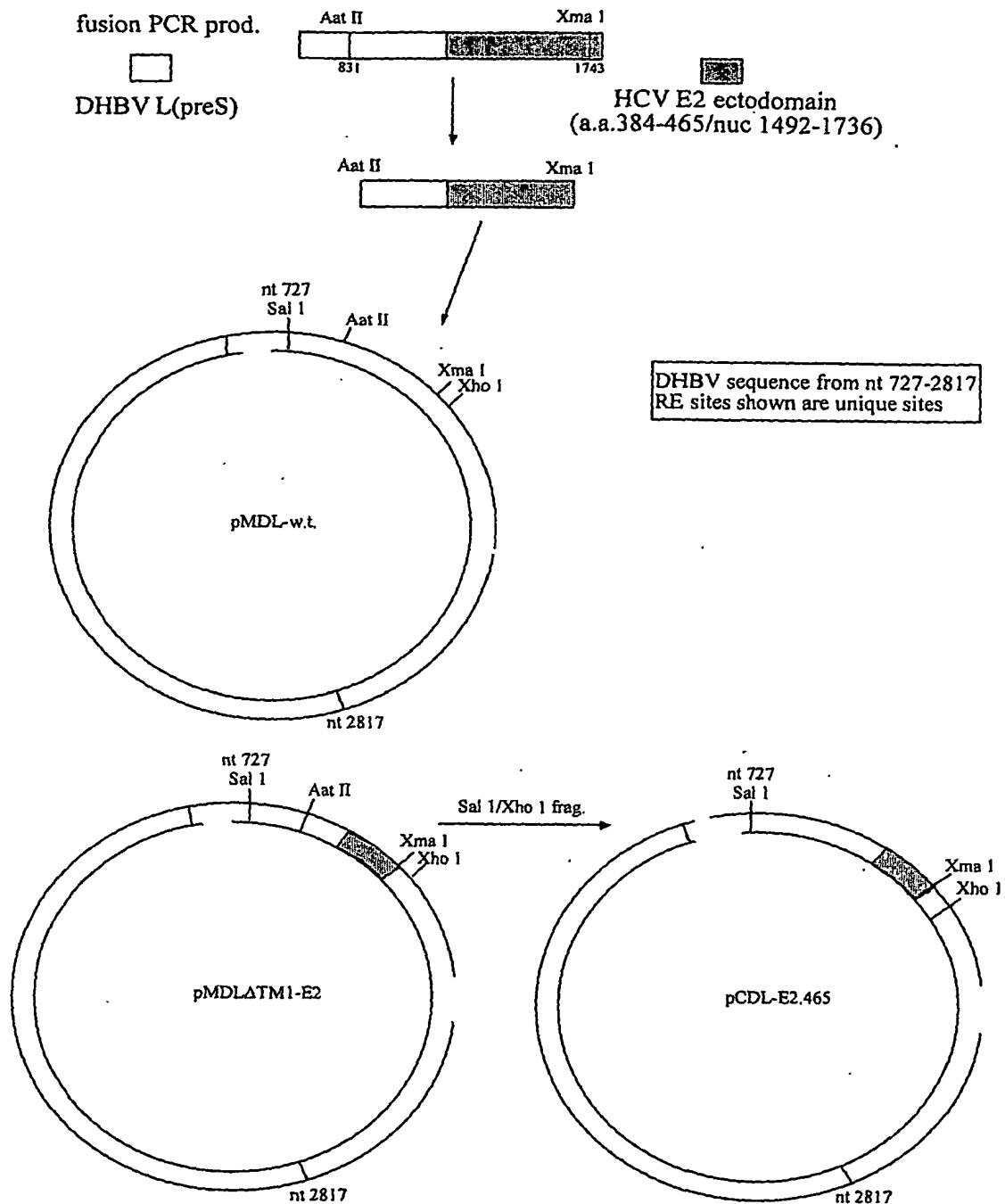
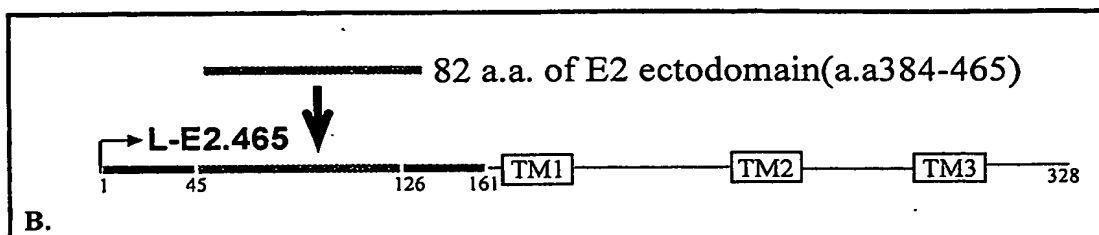
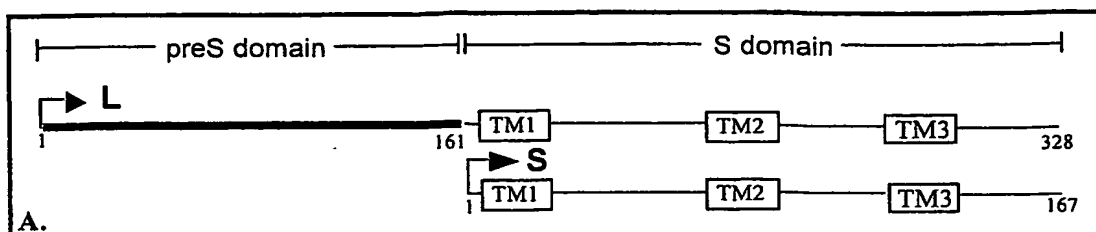


FIGURE 1

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**C.** L-E2.465 chimera is translocated across the ER membrane

trypsin	-	+	+
NP-40	-	-	+

L-E2.465 —

S —

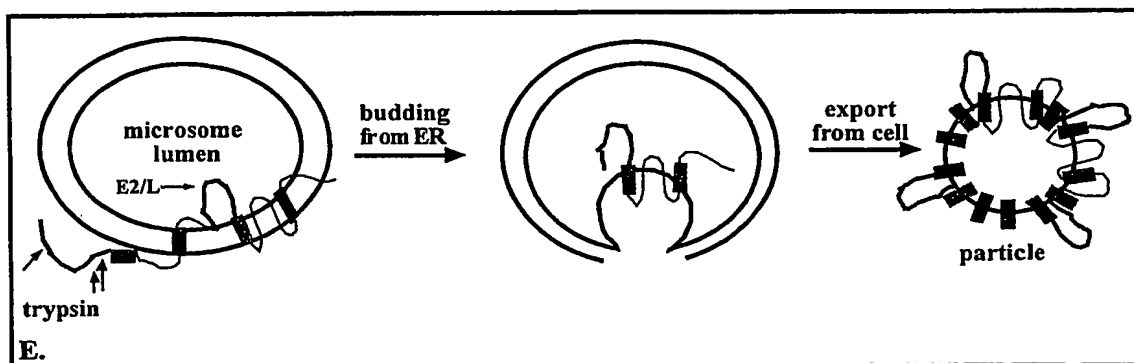
microsomes: protease protection assay

**D.** L-E2.465 chimera is assembled into particles

L-E2.465 —

S —

particles purified by sedimentation through 20% sucrose



**FIGURE 2**

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## DHBV full genome sequence (US D16 Acc. No. K01839)

1 catgctcatt tgaaagctta tgcaaaaatt aacgaggaat cactggatag ggctaggaga  
 61 ttgcttttgt ggcattacaa ctgtttactg tggggagaag ctcaagttac taactatatt  
 121 tctcgtttgc gtacttggtt gtcaactcct gagaaatata gaggtagaga tgccccgacc  
 181 attgaagcaa tctagtagacc aatccagggtg gctcagggag gcagaaaaac aactacgggt  
 241 actagaaaac ctctgtggact cgaacctaga agaagaaaag ttaaaaccac agttgtctat  
 301 gggagaagac gttcaaagtc ccgggaaagg agagccccta caccccaacg tgcgggctcc  
 361 cctctccac gtagttcgag cagccaccat agatctccct cgcctaggaa ataaattacc  
 421 tgctaggcat cacttaggta aattgtcagg actatatcaa atgaagggtt gtacttttaa  
 481 ccagaatgg aaagtaccag atatttcgga factcatttt aatttagatg tagttaatga  
 541 gtgcccttcc cgaaattgga aatatttgac tccagccaaa ttctggccca agagcatttc  
 601 ctactttcct gtccaggtag gggtaaacc aaagtatcct gacaatgtga tgcaacatga  
 661 atcaatagta ggtaaattatt taaccagggt ctatgaagca ggaatccttt ataagcggat  
 721 atctaaacat ttggtcacat ttaaaggta gccttataat tgggaacagc aacacctgtt  
 781 caatcaacat cacatttatg atggggcaac atccagcaaa atcaatggac gtcagacgga  
 841 tagaaggagg agaaatactg taaaccaac ttgccggaag gatgatccca aaagggactt  
 901 tgacatggtc aggcaagttt ccaacactag atcacgtgtt agaccatgtg caaacaatgg  
 961 aggagataaa caccctccag aatcagggag cttggcctgc tggggcggga aggagagtag  
 1021 gattatcaaa tccgactcct caagagattc ctacgcccc agtggactccc gaggaagacc  
 1081 aaaaagcacg cgaagctttt cgccgttacc aagaagaaag accaccggaa accaccacca  
 1141 ttctccgtc ttccctcctc cagtgggaagc tacaaccggg ggacgatcca ctctgggaa  
 1201 atcagtctct cctcgagact catccgctat accagtcaga accagcgggtg ccagtataa  
 1261 aaactcccc cttgaagaag aaaatgtctg gtaccttcgg gggaatacta gctggcctaa  
 1321 tcggattact ggtaagcttt ttctgttga taaaaattct agaaatactg aggaggctag  
 1381 attggtgggt gatttctctc agttctcaa agggaaaaat gcaatgcgtt ttcaagata  
 1441 ctggagccca aatctctcca cattacgtag gatcttgccc gtggggatgc ccaggatttc  
 1501 ttggaccta tctcaggctt ttatcatct tctcttaat cctgctagta gcagcaggct  
 1561 tgctgtatct gacggacaac ggggttacta tttaggaaa gctccaatgg gcgctggctt  
 1621 cagccctttt ctctccatc tcttactac tgccctcgga tccgaaatct ctctcgctt  
 1681 taacgtttgg actttcactt atatggatga ctctctctc tgccaccaa acgctcgtca  
 1741 ccttaacgca attagccacg ctgtctgctc tttttacaa gagttaggaa taagaataaa  
 1801 ctttgacaaa accacgcctt ctccggtgaa tgaataaga ttctcggtt accagattga  
 1861 tgaaaatttc atgaagattg aagaagcag atggaaagaa ttaaggactg taatcaagaa  
 1921 aataaaagta ggagaatgg atgactggaa atgtattcaa agatttgtgg ggcatttgaa  
 1981 tttgttttg ccttttacta aaggtaatat tgaatgtta aaaccaatgt atgctgctat  
 2041 tactaacc aa gtaaacttta gcttctctc atcctatagg actttgttat ataaactaac  
 2101 aatgggtgtg tgtaaattaa gaataaagcc aaagtctct gtacctttgc cacgtgtagc

FIGURE 3

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2161 tacagatgct accccaacac atggcgcaat atcccatatc accggcgggga ggcagtggt  
2221 tgcttttca aaggtcagag atatacatgt tcaggaacta ttgatgtctt gtttagccaa  
2281 gataatgatt aaaccacgtt gtctcttate tgattcaact ttgtttgcc ataagcgta  
2341 tcagacgta ccatggcatt ttgctatgtt ggccaaacaa ttgctcaaac cgatacaatt  
2401 gtactttgtc ccgagcaaat ataatcctgc tgacggccca tccaggcaca aacctcctga  
2461 ttggacggct ttccataca cccctctctc gaaagcaata tatattccac ataggctatg  
2521 tggaacttaa gaattacacc cctctcctc ggagctgctt gccaaaggat cttacgtct  
2581 acattgctgt tgctgtgtg gactgtacct ttggtatga ccattgtta tgattctgc  
2641 ttatatatgg atatcaatgc ttctagagcc ttagccaatg tgtatgatct accagatgat  
2701 ttctttcaa aaatagatga tctgttga gatgctaaag acgctttaga gccttattgg  
2761 aaatcagatt caataaagaa acatgtttg attgcaactc actttgtgga tctcattgaa  
2821 gacttctggc agactacaca gggcatgcat gaaatagccg aatcattaag agctgttata  
2881 cctcccacta ctactcctgt tccaccgggt tatcttattc agcacgagga agctgaagag  
2941 atacctttgg gagatttatt taaacaccaa gaagaaagga tagtaagttt ccaacccgac  
3001 tatccgatta cggctagaat t

**FIGURE 3 Cont.**

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DHBV L sequence (US D16) (start L atg 801; start S atg 1284)

801/1  
atg ggg caa cat cca gca aaa tca atg gac gtc aga cgg ata gaa gga gga gaa gaa ata ctg  
M G Q H P A K S M D V R R I E G G G E I L

861/21  
tta aac caa ctt gcc gga agg atg atc cca aaa ggg act ttg aca tgg tca ggc aag ttt  
L N Q L A G R M I P K G T L T W S G K F

921/41  
cca aca cta gat cac gtg tta gac cat gtg caa aca atg gag gag ata aac acc ctc cag  
P T L D H V L D H V Q T M E E I N T L Q

981/61  
aat cag gga gct tgg cct gct ggg gcg gga agg aga gta gga tta tca aat ccg act cct  
N Q G A W P A G A G R R V G L S N P T P

1041/81  
caa gag att cct cag ccc cag tgg act ccc gag gaa gac caa aaa gca cgc gaa gct ttt  
Q E I P Q P Q W T P E E D Q K A R E A F

1101/101  
cgc cgt tat caa gaa gaa aga cca ccg gaa acc acc acc att cct ccg tct tcc cct cct  
R R Y Q E E R P P E T T T I P P S S P P

1161/121  
cag tgg aag cta caa ccc ggg gac gat cca ctc ctg gga aat cag tct ctc ctc gag act  
Q W K L Q P G D D P L L G N Q S L L E T

1221/141  
831/11  
891/31  
951/51  
1011/71  
1071/91  
1131/111  
1191/131  
1251/151

## FIGURE 4

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cat ccg cta tac cag tca gaa cca gcg gtg cca gtg ata aaa act ccc ccc ttg aag aag  
 H P L Y Q S E P A V P V I K T P P L K K  
 1281/161  
 aaa atg tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta ctg gta agc ttt  
 K M S G T F G I L A G L I G L L V S F  
 1341/181  
 ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta gat tgg tgg att tct ctc  
 F L L I K I L E I L R R L D W W I S L  
 1401/201  
 agt tct cca aag gga aaa atg caa tgc gct ttc caa gat act gga gcc caa atc tct cca  
 S S P K G K M Q C A F Q D T G A Q I S P  
 1461/221  
 cat tac gta gga tct tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt  
 H Y V G S C P W G C P G F L W T Y L R L  
 1521/241  
 ttt atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg acg gac aac  
 F I I F L L I L I L V A A G L L Y L T D N  
 1581/261  
 ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc tca gcc ctt ttc tcc atc  
 G S T I L G K L Q W A S V S A L F S I  
 1641/281  
 tct tca cta ctg ccc tcg gat ccg aaa tct ctc gtc gct tta acg ttt gga ctt tca ctt  
 S S L L P S D P K S L V A L T F G L S L  
 1701/301  
 1731/311

FIGURE 4 Cont.

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```

ata tgg atg act tcc tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg
I W M T S S S S A T Q T L V T L A T
1761/321
ctg tct gct ctt ttt tac aag agt tag
L S A L F Y K S *
1791/331

```

FIGURE 4 Cont.

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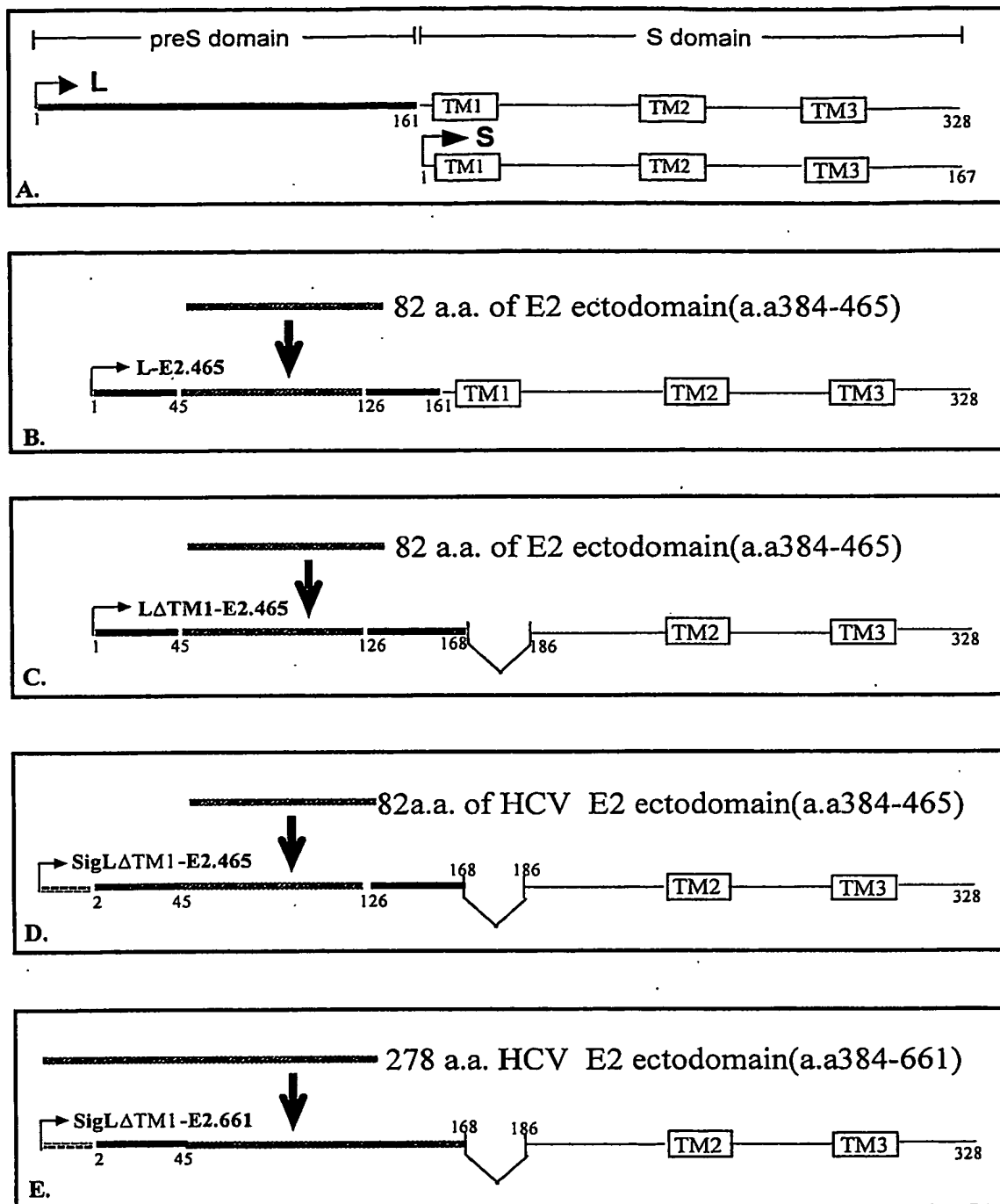


FIGURE 5



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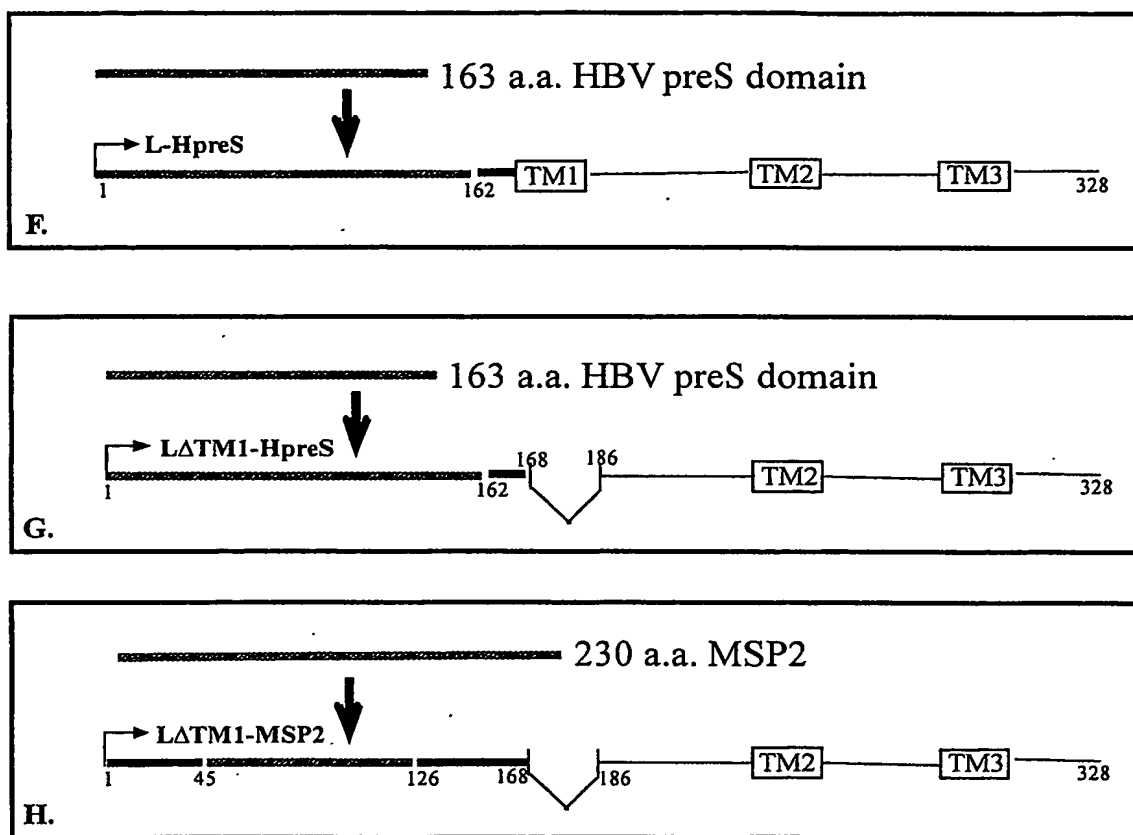


FIGURE 5 cont.

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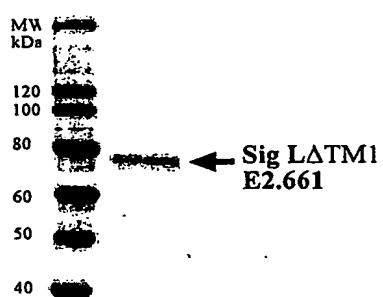
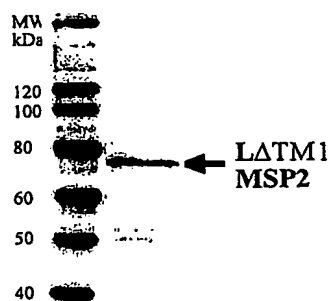
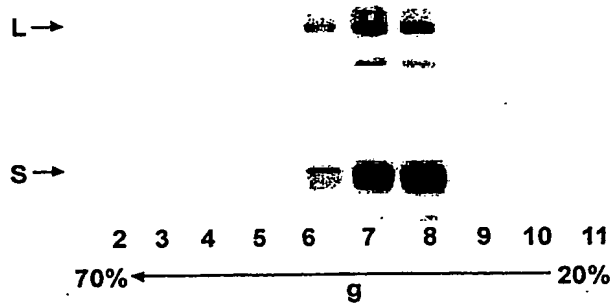
A. Sig $\Delta$ TM1-E2.661 membrane fractionB.  $\Delta$ TM1-MSP2 membrane fraction

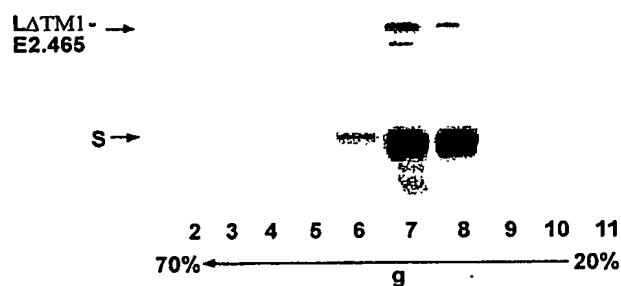
FIGURE 6

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## A. DL/S VLPs: sucrose step gradient profile



## B. DLATM1-E2.465 VLPs: sucrose step gradient profile



## C. DLATM1-HpreS VLPs: sucrose step gradient profile

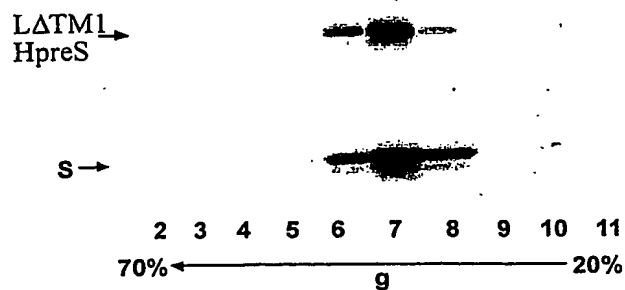
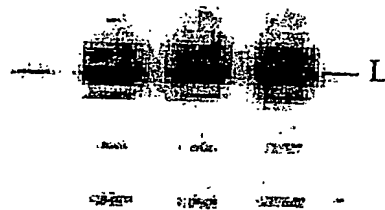


FIGURE 7

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rat sera:sequential bleeds  
pre 1 2 4 5



preS reactivity

**FIGURE 8**